

0570
1011

#3

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/676,436

DATE: 11/07/2001

TIME: 15:14:33

Input Set : A:\RTS-0169_Seq_ASCII.txt

Output Set: N:\CRF3\11072001\I676436.raw

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3 <110> APPLICANT: Donna T. Ward
4      William Gaarde
5      Brett P. Monia
6      Jacqueline Wyatt
8 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK4 EXPRESSION
10 <130> FILE REFERENCE: RTS-0169
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/676,436
C--> 12 <141> CURRENT FILING DATE: 2000-09-29
12 <160> NUMBER OF SEQ ID NOS: 89
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16 <211> LENGTH: 20
17 <212> TYPE: DNA
18 <213> ORGANISM: Artificial Sequence ✓
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20 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓
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23 tccgtcatcg ctcctcaggg
26 <210> SEQ ID NO: 2
27 <211> LENGTH: 20
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence ✓
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31 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓
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34 atgcattctg cccccaagga
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38 <211> LENGTH: 4990
39 <212> TYPE: DNA
40 <213> ORGANISM: Homo sapiens
42 <220> FEATURE:
43 <221> NAME/KEY: CDS
44 <222> LOCATION: (1)...(4476)
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48 Leu Glu Asp Phe Ser Asp Glu Thr Asn Thr Glu Asn Leu Tyr Gly Thr
49 1      5      10      15
51 tct ccc ccc agc aca cct cga cag atg aaa cgc atg tca acc aaa cat      96
52 Ser Pro Pro Ser Thr Pro Arg Gln Met Lys Arg Met Ser Thr Lys His
53      20      25      30
55 cag agg aat aat gtg ggg agg cca gcc agt cgg tct aat ttg aaa gaa      144
56 Gln Arg Asn Asn Val Gly Arg Pro Ala Ser Arg Ser Asn Leu Lys Glu
57      35      40      45
59 aaa atg aat gca cca aat cag cct cca cat aaa gac act gga aaa aca      192
60 Lys Met Asn Ala Pro Asn Gln Pro Pro His Lys Asp Thr Gly Lys Thr
61      50      55      60
63 gtg gag aat gtg gaa gaa tac agc tat aag cag gag aaa aag atc cga      240
64 Val Glu Asn Val Glu Glu Tyr Ser Tyr Lys Gln Glu Lys Lys Ile Arg

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ENTERED

20
ENTERED

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65	65	70	75	80	
67	gca gct ctt aga aca aca gag cgt gat cat aaa aaa aat gta cag tgc				288
68	Ala Ala Leu Arg Thr Thr Glu Arg Asp His Lys Lys Asn Val Gln Cys				
69		85	90	95	
71	tca ttc atg tta gac tca gtg ggt gga tct ttg cca aaa aaa tca att				336
72	Ser Phe Met Leu Asp Ser Val Gly Gly Ser Leu Pro Lys Lys Ser Ile				
73		100	105	110	
75	cca gat gtg gat ctc aat aag cct tac ctc agc ctt ggc tgt agc aat				384
76	Pro Asp Val Asp Leu Asn Lys Pro Tyr Leu Ser Leu Gly Cys Ser Asn				
77		115	120	125	
79	gct aag ctt cca gta tct gtg ccc atg cct ata gcc aga cct gca cgc				432
80	Ala Lys Leu Pro Val Ser Val Pro Met Pro Ile Ala Arg Pro Ala Arg				
81		130	135	140	
83	cag act tct agg act gac tgt cca gca gat cgt tta aag ttt ttt gaa				480
84	Gln Thr Ser Arg Thr Asp Cys Pro Ala Asp Arg Leu Lys Phe Phe Glu				
85	145	150	155	160	
87	act tta cga ctt ttg cta aag ctt acc tca gtc tca aag aaa aaa gac				528
88	Thr Leu Arg Leu Leu Leu Lys Leu Thr Ser Val Ser Lys Lys Lys Asp				
89		165	170	175	
91	agg gag caa aga gga caa gaa aat acg tct ggt ttc tgg ctt aac cga				576
92	Arg Glu Gln Arg Gly Gln Glu Asn Thr Ser Gly Phe Trp Leu Asn Arg				
93		180	185	190	
95	tct aac gaa ctg atc tgg tta gag cta caa gcc tgg cat gca gga cgg				624
96	Ser Asn Glu Leu Ile Trp Leu Glu Leu Gln Ala Trp His Ala Gly Arg				
97		195	200	205	
99	aca att aac gac cag gac ttc ttt tta tat aca gcc cgt caa gcc atc				672
100	Thr Ile Asn Asp Gln Asp Phe Phe Leu Tyr Thr Ala Arg Gln Ala Ile				
101		210	215	220	
103	cca gat att att aat gaa atc ctt act ttc aaa gtc gac tat ggg agc				720
104	Pro Asp Ile Ile Asn Glu Ile Leu Thr Phe Lys Val Asp Tyr Gly Ser				
105	225	230	235	240	
107	ttc gcc ttt gtt aga gat aga gct ggt ttt aat ggt act tca gta gaa				768
108	Phe Ala Phe Val Arg Asp Arg Ala Gly Phe Asn Gly Thr Ser Val Glu				
109		245	250	255	
111	ggg cag tgc aaa gcc act cct gga aca aag att gta ggt tac tca aca				816
112	Gly Gln Cys Lys Ala Thr Pro Gly Thr Lys Ile Val Gly Tyr Ser Thr				
113		260	265	270	
115	cat cat gag cat ctc caa cgc cag agg gtc tca ttt gag cag gta aaa				864
116	His His Glu His Leu Gln Arg Gln Arg Val Ser Phe Glu Gln Val Lys				
117		275	280	285	
119	cgg ata atg gag ctg cta gag tac ata gaa gca ctt tat cca tca ttg				912
120	Arg Ile Met Glu Leu Leu Glu Tyr Ile Glu Ala Leu Tyr Pro Ser Leu				
121		290	295	300	
123	cag gct ctt cag aag gac tat gaa aaa tat gct gca aaa gac ttc cag				960
124	Gln Ala Leu Gln Lys Asp Tyr Glu Lys Tyr Ala Ala Lys Asp Phe Gln				
125	305	310	315	320	
127	gac agg gtg cag gca ctc tgt ttg tgg tta aac atc aca aaa gac tta				1008
128	Asp Arg Val Gln Ala Leu Cys Leu Trp Leu Asn Ile Thr Lys Asp Leu				
129		325	330	335	

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131	aat	cag	aaa	tta	agg	att	atg	ggc	act	gtt	ttg	ggc	atc	aag	aat	tta	1056
132	Asn	Gln	Lys	Leu	Arg	Ile	Met	Gly	Thr	Val	Leu	Gly	Ile	Lys	Asn	Leu	
133				340					345					350			
135	tca	gac	att	ggc	tgg	cca	gtg	ttt	gaa	atc	cct	tcc	cct	cga	cca	tcc	1104
136	Ser	Asp	Ile	Gly	Trp	Pro	Val	Phe	Glu	Ile	Pro	Ser	Pro	Arg	Pro	Ser	
137				355					360					365			
139	aaa	ggt	aat	gag	ccg	gag	tat	gag	ggt	gat	gac	aca	gaa	gga	gaa	tta	1152
140	Lys	Gly	Asn	Glu	Pro	Glu	Tyr	Glu	Gly	Asp	Asp	Thr	Glu	Gly	Glu	Leu	
141				370					375				380				
143	aag	gag	ttg	gaa	agt	agt	acg	gat	gag	agt	gaa	gaa	gaa	caa	atc	tct	1200
144	Lys	Glu	Leu	Glu	Ser	Ser	Thr	Asp	Glu	Ser	Glu	Glu	Glu	Gln	Ile	Ser	
145	385					390					395					400	
147	gat	cct	agg	gta	ccg	gaa	atc	aga	cag	ccc	ata	gat	aac	agc	ttc	gac	1248
148	Asp	Pro	Arg	Val	Pro	Glu	Ile	Arg	Gln	Pro	Ile	Asp	Asn	Ser	Phe	Asp	
149					405					410					415		
151	atc	cag	tcg	cgg	gac	tgc	ata	tcc	aag	aag	ctt	gag	agg	ctc	gaa	tct	1296
152	Ile	Gln	Ser	Arg	Asp	Cys	Ile	Ser	Lys	Lys	Leu	Glu	Arg	Leu	Glu	Ser	
153				420					425					430			
155	gag	gat	gat	tct	ctt	ggc	tgg	gga	gca	cca	gac	tgg	agc	aca	gaa	gca	1344
156	Glu	Asp	Asp	Ser	Leu	Gly	Trp	Gly	Ala	Pro	Asp	Trp	Ser	Thr	Glu	Ala	
157				435					440					445			
159	ggc	ttt	agt	aga	cat	tgt	ctg	act	tct	att	tat	aga	cca	ttt	gta	gac	1392
160	Gly	Phe	Ser	Arg	His	Cys	Leu	Thr	Ser	Ile	Tyr	Arg	Pro	Phe	Val	Asp	
161				450					455				460				
163	aaa	gca	ctg	aag	cag	atg	ggg	tta	aga	aag	tta	att	tta	aga	ctt	cac	1440
164	Lys	Ala	Leu	Lys	Gln	Met	Gly	Leu	Arg	Lys	Leu	Ile	Leu	Arg	Leu	His	
165	465					470					475					480	
167	aag	cta	atg	gat	ggt	tcc	ttg	caa	agg	gca	cgt	ata	gca	ttg	gta	aag	1488
168	Lys	Leu	Met	Asp	Gly	Ser	Leu	Gln	Arg	Ala	Arg	Ile	Ala	Leu	Val	Lys	
169					485					490					495		
171	aac	gat	cgt	cca	gtg	gag	ttt	tct	gaa	ttt	cca	gat	ccc	atg	tgg	ggt	1536
172	Asn	Asp	Arg	Pro	Val	Glu	Phe	Ser	Glu	Phe	Pro	Asp	Pro	Met	Trp	Gly	
173				500					505					510			
175	tca	gat	tat	gtg	cag	ttg	tca	agg	aca	cca	cct	tca	tct	gag	gag	aaa	1584
176	Ser	Asp	Tyr	Val	Gln	Leu	Ser	Arg	Thr	Pro	Pro	Ser	Ser	Glu	Glu	Lys	
177				515					520					525			
179	tgc	agt	gct	gtg	tcg	tgg	gag	gag	ctg	aag	gcc	atg	gat	tta	cct	tca	1632
180	Cys	Ser	Ala	Val	Ser	Trp	Glu	Glu	Leu	Lys	Ala	Met	Asp	Leu	Pro	Ser	
181				530					535				540				
183	ttc	gaa	cct	gcc	ttc	cta	gtt	ctc	tgc	cga	gtc	ctt	ctg	aat	gtc	ata	1680
184	Phe	Glu	Pro	Ala	Phe	Leu	Val	Leu	Cys	Arg	Val	Leu	Leu	Asn	Val	Ile	
185	545					550					555					560	
187	cat	gag	tgt	ctg	aag	tta	aga	ttg	gag	cag	aga	cct	gct	gga	gaa	cca	1728
188	His	Glu	Cys	Leu	Lys	Leu	Arg	Leu	Glu	Gln	Arg	Pro	Ala	Gly	Glu	Pro	
189					565					570					575		
191	tct	ctc	ttg	agt	att	aag	cag	ctg	gtg	aga	gag	tgt	aag	gag	gtc	ctg	1776
192	Ser	Leu	Leu	Ser	Ile	Lys	Gln	Leu	Val	Arg	Glu	Cys	Lys	Glu	Val	Leu	
193				580					585					590			
195	aag	ggc	ggc	ctg	ctg	atg	aag	cag	tac	tac	cag	ttc	atg	ctg	cag	gag	1824

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196 Lys Gly Gly Leu Leu Met Lys Gln Tyr Tyr Gln Phe Met Leu Gln Glu
197          595          600          605
199 gtt ctg gag gac ttg gag aag ccc gac tgc aac att gac gct ttt gaa 1872
200 Val Leu Glu Asp Leu Glu Lys Pro Asp Cys Asn Ile Asp Ala Phe Glu
201      610          615          620
203 gag gat cta cat aaa atg ctt atg gtg tat ttt gat tac atg aga agc 1920
204 Glu Asp Leu His Lys Met Leu Met Val Tyr Phe Asp Tyr Met Arg Ser
205 625          630          635          640
207 tgg atc caa atg cta cag caa tta cct caa gca tcg cat agt tta aaa 1968
208 Trp Ile Gln Met Leu Gln Gln Leu Pro Gln Ala Ser His Ser Leu Lys
209          645          650          655
211 aat ctg tta gaa gaa gaa tgg aat ttc acc aaa gaa ata act cat tac 2016
212 Asn Leu Leu Glu Glu Glu Trp Asn Phe Thr Lys Glu Ile Thr His Tyr
213      660          665          670
215 ata cgg gga gga gaa gca cag gcc ggg aag ctt ttc tgt gac att gca 2064
216 Ile Arg Gly Gly Glu Ala Gln Ala Gly Lys Leu Phe Cys Asp Ile Ala
217      675          680          685
219 gga atg ctg ctg aaa tct aca gga agt ttt tta gaa ttt ggc tta cag 2112
220 Gly Met Leu Leu Lys Ser Thr Gly Ser Phe Leu Glu Phe Gly Leu Gln
221      690          695          700
223 gag agc tgt gct gaa ttt tgg act agt gcg gat gac agc agt gct tcc 2160
224 Glu Ser Cys Ala Glu Phe Trp Thr Ser Ala Asp Asp Ser Ser Ala Ser
225 705          710          715          720
227 gac gaa atc agg agg tct gtt ata gag atc agt cga gcc ctg aag gag 2208
228 Asp Glu Ile Arg Arg Ser Val Ile Glu Ile Ser Arg Ala Leu Lys Glu
229          725          730          735
231 ctc ttc cat gaa gcc aga gaa agg gct tcc aaa gca ctt gga ttt gct 2256
232 Leu Phe His Glu Ala Arg Glu Arg Ala Ser Lys Ala Leu Gly Phe Ala
233      740          745          750
235 aaa atg ttg aga aag gac ctg gaa ata gca gca gaa ttc agg ctt tca 2304
236 Lys Met Leu Arg Lys Asp Leu Glu Ile Ala Ala Glu Phe Arg Leu Ser
237      755          760          765
239 gcc cca gtt aga gac ctc ctg gat gtt ctg aaa tca aaa cag tat gtc 2352
240 Ala Pro Val Arg Asp Leu Leu Asp Val Leu Lys Ser Lys Gln Tyr Val
241      770          775          780
243 aag gtg caa att cct ggg tta gaa aac ttg caa atg ttt gtt cca gac 2400
244 Lys Val Gln Ile Pro Gly Leu Glu Asn Leu Gln Met Phe Val Pro Asp
245 785          790          795          800
247 act ctt gct gag gag aag agt att att ttg cag tta ctc aat gca gct 2448
248 Thr Leu Ala Glu Glu Lys Ser Ile Ile Leu Gln Leu Leu Asn Ala Ala
249          805          810          815
251 gca gga aag gac tgt tca aaa gat tca gat gac gta ctc atc gat gcc 2496
252 Ala Gly Lys Asp Cys Ser Lys Asp Ser Asp Asp Val Leu Ile Asp Ala
253      820          825          830
255 tat ctg ctt ctg acc aag cac ggt gat cga gcc cgt gat tca gag gac 2544
256 Tyr Leu Leu Leu Thr Lys His Gly Asp Arg Ala Arg Asp Ser Glu Asp
257      835          840          845
259 agc tgg ggc acc tgg gag gca cag cct gtc aaa gtc gtg cct cag gtg 2592
260 Ser Trp Gly Thr Trp Glu Ala Gln Pro Val Lys Val Val Pro Gln Val

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261	850	855	860	
263	gag act gtt gac acc ctg aga agc atg cag gtg gat aat ctt tta cta			2640
264	Glu Thr Val Asp Thr Leu Arg Ser Met Gln Val Asp Asn Leu Leu Leu			
265	865	870	875	880
267	gtt gtc atg cag tct gcg cat ctc aca att cag aga aaa gct ttc cag			2688
268	Val Val Met Gln Ser Ala His Leu Thr Ile Gln Arg Lys Ala Phe Gln			
269		885	890	895
271	cag tcc att gag gga ctt atg act ctg tgc cag gag cag aca tcc agt			2736
272	Gln Ser Ile Glu Gly Leu Met Thr Leu Cys Gln Glu Gln Thr Ser Ser			
273		900	905	910
275	cag ccg gtc atc gcc aaa gct ttg cag cag ctg aag aat gat gca ttg			2784
276	Gln Pro Val Ile Ala Lys Ala Leu Gln Gln Leu Lys Asn Asp Ala Leu			
277		915	920	925
279	gag cta tgc aac agg ata agc aat gcc att gac cgc gtg gac cac atg			2832
280	Glu Leu Cys Asn Arg Ile Ser Asn Ala Ile Asp Arg Val Asp His Met			
281		930	935	940
283	ttc aca tca gaa ttt gat gct gag gtt gat gaa tct gaa tct gtc acc			2880
284	Phe Thr Ser Glu Phe Asp Ala Glu Val Asp Glu Ser Glu Ser Val Thr			
285		945	950	955
287	ttg caa cag tac tac cga gaa gca atg att cag ggg tac aat ttt gga			2928
288	Leu Gln Gln Tyr Tyr Arg Glu Ala Met Ile Gln Gly Tyr Asn Phe Gly			
289		965	970	975
291	ttt gag tat cat aaa gaa gtt gtt cgt ttg atg tct ggg gag ttt aga			2976
292	Phe Glu Tyr His Lys Glu Val Val Arg Leu Met Ser Gly Glu Phe Arg			
293		980	985	990
295	cag aag ata gga gac aaa tat ata agc ttt gcc cgg aag tgg atg aat			3024
296	Gln Lys Ile Gly Asp Lys Tyr Ile Ser Phe Ala Arg Lys Trp Met Asn			
297		995	1000	1005
299	tat gtc ctg act aaa tgt gag agt ggt aga ggt aca aga ccc agg tgg			3072
300	Tyr Val Leu Thr Lys Cys Glu Ser Gly Arg Gly Thr Arg Pro Arg Trp			
301		1010	1015	1020
303	gcg act caa gga ttt gat ttt cta caa gca att gaa cct gcc ttt att			3120
304	Ala Thr Gln Gly Phe Asp Phe Leu Gln Ala Ile Glu Pro Ala Phe Ile			
305		1025	1030	1035
307	tca gct tta cca gaa gat gac ttc ttg agt tta caa gcc ttg atg aat			3168
308	Ser Ala Leu Pro Glu Asp Asp Phe Leu Ser Leu Gln Ala Leu Met Asn			
309		1045	1050	1055
311	gaa tgc att ggc cat gtc ata gga aaa cca cac agt cct gtt aca ggt			3216
312	Glu Cys Ile Gly His Val Ile Gly Lys Pro His Ser Pro Val Thr Gly			
313		1060	1065	1070
315	ttg tac ctt gcc att cat cgg aac agc ccc cgt cct atg aag gta cct			3264
316	Leu Tyr Leu Ala Ile His Arg Asn Ser Pro Arg Pro Met Lys Val Pro			
317		1075	1080	1085
319	cga tgc cat agt gac cct cct aac cca cac ctc att atc ccc act cca			3312
320	Arg Cys His Ser Asp Pro Pro Asn Pro His Leu Ile Ile Pro Thr Pro			
321		1090	1095	1100
323	gag gga ttc agg ggt tcc agc gtt cct gaa aat gat cga ttg gct tcc			3360
324	Glu Gly Phe Arg Gly Ser Ser Val Pro Glu Asn Asp Arg Leu Ala Ser			
325		1105	1110	1115
				1120

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:20 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:31 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:420 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
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